Amendments to the Specification:

Please replace paragraph [0013] with the following paragraph:

[0013] Structural predictions based on mathematical calculations derived from experimental data such as protein crystal structures ~~(Pfam: http://hits.isb-sib.ch/cgi-bin/PFSCAN?)~~ show that all previously known branching enzymes from higher plants have two domains: an alpha-amylase domain and an iso-amylase domain. Here, the iso-amylase domain lies closer to the N-terminus of the protein than the alpha-amylase domain.

Please replace paragraph [0037] with the following paragraph:

[0037] With the help of the Pfam database (Batemann et al., 2002, Nucleic Acids Research 30, 276-280; accessible via ~~http://www.sanger.ac.uk/Software/Pfam/, http://www.cgb.ki.se/Pfam/; http://pfam.jouy.inra.fr/ or http://pfam.wustl.edu/)~~ the Wellcome Trust Sanger Institute website or the Institute National de la Recherche Agronomique website), it is possible for the person skilled in the art to determine whether amino acid sequences already have known domains (e.g. an iso-amylase domain and/or an alpha-amylase domain). Pfam is a database put together by experts, which classifies amino acid sequences into so-called families. Here, the assignment of an amino acid sequence to a family is carried out on the basis of so-called domains, which are to be looked upon as functional and structural components of proteins. A domain is defined as a structural unit or a repeatedly occurring amino acid sequence unit, which can occur in proteins with widely different functions. Along with information relating to the amino acid sequence of known proteins, further knowledge (e.g. evidence of the enzymatic activity, crystal structure data) is also used for the assignment of a protein to a family. Each family is assigned a name and an "accession" number (e.g. Name: Isoamylase_N, acc: PF02922). A constituent part of each family in the Pfam database is, amongst other things, a so-called "seed alignment". The "seed alignment" contains the amino acid sequences of representative proteins of a family. Starting from "seed alignments", a so-called profile HMM ("profile Hidden Markov Model"; overview article in: Durbin et al., "Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids", Cambridge University Press, 1998, ISBN 0-521-62041-4) is produced using the HMMER 2 software (freely available ~~under http://hmmer.wustl.edu/~~ on the world wide web). The HMMs produced have names and are stored in the Pfam database specifically for the correspondingly assigned domains. In contrast to classical, multiple "alignments" (e.g. produced using the Clustal W program or the Blossum62 algorithm),

HMMs are based on a valid statistical theory (Bayes theory of conditional probability, Markoff chains) and enable an interrogation sequence (query) to be assigned to a family based on the use of position-specific evaluation matrices. This enables an assignment to be made even when there are considerable differences in the amino acid sequences between the interrogation sequence (query) and a comparison sequence (e.g. amino acid sequence entry in a database).

Please replace paragraph [0038] with the following paragraph:

[0038] The domain structure of the amino acid sequence concerned can be determined by means of a comparison of the HMMs stored in the Pfam database with amino acid sequences, which are entered as a so-called interrogation sequence (query) (e.g. ~~under http://hits.isb-sib.ch/cgi-bin/PFSCAN?~~ myhits motif scan, available on the world wide web).

Please replace paragraph [0040] with the following paragraph:

[0040] In conjunction with the present invention, the term "alpha-amylase domain" is to be understood to mean a Pfam alpha-amylase domain (acc: Pf00128). At the same time, the HMM describing this Pfam alpha-amylase domain is to be produced with the HMMER 2 [2.3.1] software, starting from a "seed alignment", which contains the amino acid sequences shown in Table 2. Here, the "seed alignment" is produced by means of HMM_simulated_annealing ~~(http://www.pse.edu/general/software/packages/hmmer/manual/node11.html#SECTION00321000000000000000~~ available on the world wide web). The following settings must be chosen to produce the appropriate HMM: Build Method of HMM: hmmbuild-F HMM_Is, hmmcalibrate-seed 0 HMM_Is; Gathering cutoff: -82.0-82.0; Trusted cutoff: -81.7-81.7; Noise cutoff: -82.7-82.7). Further information for producing the HMM of the Pfam alpha-amylase domain (acc: Pf00128) is given in Table 4.

Please replace paragraph [0064] with the following paragraph:

[0064] The examination of databases, such as are made available, for example, by EMBL ~~(http://www.ebi.ac.uk/Tools/index.htm)~~ or NCBI (National Center for Biotechnology Information, ~~http://www.ncbi.nlm.nih.gov/~~), can also be used for identifying homologous sequences, which code for a Class 3 branching enzyme. In this case, one or more sequences are specified as a so-called query. This query sequence is then compared by means of statistical computer programs with sequences, which are contained in the selected databases. Such database

queries (e.g. blast or fasta searches) are known to the person skilled in the art and can be carried out by various providers. If such a database query is carried out, e.g. at the NCBI (National Center for Biotechnology Information website, ~~http://www.ncbi.nlm.nih.gov/~~), then the standard settings, which are specified for the particular comparison inquiry, should be used. For protein sequence comparisons (blastp), these are the following settings: Limit entrez = not activated; Filter = low complexity activated; Expect value = 10; word size = 3; Matrix = BLOSUM62; Gap costs: Existence = 11, Extension = 1.

Please replace paragraph [0077] with the following paragraph:

[0077] In conjunction with the present invention, the term "identity" means a sequence identity over the whole length of the coding region of at least 60%, in particular an identity of at least 70%, preferably greater than 80%, particularly preferably greater than 90% and especially of at least 95%. In conjunction with the present invention, the term "identity" is to be understood to mean the number of amino acids/nucleotides (identity) corresponding with other proteins/nucleic acids, expressed as a percentage. Identity is preferably determined by comparing the Seq. ID NO 4 or SEQ ID NO 3 with other proteins/nucleic acids with the help of computer programs. If sequences that are compared with one another have different lengths, the identity is to be determined in such a way that the number of amino acids, which have the shorter sequence in common with the longer sequence, determines the percentage quotient of the identity. Preferably, identity is determined by means of the computer program ClustalW, which is well known and available to the public (Thompson et al., Nucleic Acids Research 22 (1994), 4673-4680). ClustalW is made publicly available by Julie Thompson (Thompson@EMBL-Heidelberg.DE) and Toby Gibson (Gibson@EMBL-Heidelberg.DE), European Molecular Biology Laboratory, Meyerhofstrasse 1, D 69117 Heidelberg, Germany. ClustalW can also be downloaded from different Internet sites, including the IGBMC (Institut de Génétique et de Biologie Moléculaire et Cellulaire, B.P.163, 67404 Illkirch Cedex, France; ~~ftp://ftp.igbmc.u-strasbg.fr/pub/~~) and the EBI (~~ftp://ftp.ebi.ac.uk/pub/software/~~) as well as from all mirrored Internet sites of the EBI (European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK).

Please insert the following paragraphs after paragraph [0144]:

Table 1 shows the amino acid sequences, contained in the "seed alignment," that are used for producing the HMM describing for the Pfam isoamylase domain (PF 02922).

Table 2 shows the amino acid sequences, contained in the "seed alignment," that are used for producing the HMM describing for the Pfam alpha-amylase domain (PF 00128).

Table 3 shows information for producing the HMM for the Pfam isoamylase domain (PF 02922).

Table 4 shows information for producing the HMM for the Pfam alpha-amylase domain (PF 00128).

Please replace the Table number in paragraph [0167] as follows:

[0167] Table ~~1~~ A

Please replace paragraph [0173] with the following paragraph:

[0173] By sequence comparisons with different branching enzymes, a domain was identified, with the help of which EST databases were examined. In doing so, the EST TC73137 (TIGR database~~; http://www.tigr.org/tigr-scripts/tgi/tc_report.pl?tc=TC73137&species=potato~~) from potato was identified.